



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 163643

TO: Nita M Minnifield
Location: REM/3C01/3C18
Art Unit: 1645
Monday, August 29, 2005

Case Serial Number: 10/613228

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

*Reviewed
10/05
mm*



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STIC-Biotech/ChemLib

163643

From: Minnifield, Nita
Sent: Wednesday, August 24, 2005 12:37 PM
To: STIC-Biotech/ChemLib
Subject: interference sequence search request

10/613228

STIC

Please do an interference sequence search on SEQ ID NO: 1 of this application.

Please show first 30 results/alignments.

Please provide a paper copy of all results.

Thanks,
Minnifield,
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2005, 22:52:19 ; Search time 373 Seconds
(Without alignments)
385.920 Million cell updates/sec

Title: US-10-613-228a-1
Perfect score: 1 tcgcgttccttcgtcgttccttc 22
Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCR_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEM_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US08_NEM_PUB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09_NEM_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10K_PUBCOMB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US10L_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US10M_PUBCOMB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US10N_PUBCOMB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US10O_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	18	US-10-613-228a-1
2	22	100.0	22	20	US-10-616-220-152
3	22	100.0	22	21	US-10-644-052A-290
4	20.4	92.7	618	20	US-10-363-345A-34257
5	20.4	92.7	618	20	US-10-363-345A-34258
6	20.4	92.7	618	21	US-10-363-463A-34257
7	20.4	92.7	618	21	US-10-363-463A-34258

8	20.4	92.7	619	20	US-10-363-345A-40287	Sequence 40287, A
9	20.4	92.7	619	20	US-10-363-345A-40288	Sequence 40288, A
10	20.4	92.7	619	21	US-10-363-463A-40287	Sequence 40287, A
11	20.4	92.7	619	21	US-10-363-463A-40288	Sequence 40288, A
12	20.4	92.7	761	20	US-10-363-345A-2025	Sequence 2025, Ap
13	20.4	92.7	761	20	US-10-363-345A-2026	Sequence 2026, Ap
14	20.4	92.7	761	21	US-10-363-463A-2025	Sequence 2025, Ap
15	20.4	92.7	761	21	US-10-363-463A-2026	Sequence 2026, Ap
16	20.4	92.7	1024	20	US-10-363-345A-7203	Sequence 7203, Ap
17	20.4	92.7	1024	20	US-10-363-345A-7204	Sequence 7204, Ap
18	20.4	92.7	1024	21	US-10-363-463A-7203	Sequence 7203, Ap
19	20.4	92.7	1024	21	US-10-363-463A-7204	Sequence 7204, Ap
20	19.4	88.2	511	20	US-10-363-345A-28015	Sequence 28015, A
21	19.4	88.2	511	20	US-10-363-345A-28016	Sequence 28016, A
22	19.4	88.2	511	21	US-10-363-463A-28015	Sequence 28015, A
23	19.4	88.2	511	21	US-10-363-463A-28016	Sequence 28016, A
24	19.4	88.2	523	20	US-10-363-345A-35059	Sequence 35059, A
25	19.4	88.2	523	20	US-10-363-345A-35060	Sequence 35060, A
26	19.4	88.2	523	21	US-10-363-463A-35059	Sequence 35059, A
27	19.4	88.2	523	21	US-10-363-463A-35060	Sequence 35060, A
28	19.4	88.2	524	20	US-10-363-345A-40325	Sequence 40325, A
29	19.4	88.2	524	20	US-10-363-345A-40326	Sequence 40326, A
30	19.4	88.2	524	21	US-10-363-463A-40325	Sequence 40325, A
31	19.4	88.2	524	21	US-10-363-463A-40326	Sequence 40326, A
32	19.4	88.2	610	20	US-10-363-345A-23153	Sequence 23153, A
33	19.4	88.2	610	20	US-10-363-345A-23154	Sequence 23154, A
34	19.4	88.2	610	21	US-10-363-463A-23153	Sequence 23153, A
35	19.4	88.2	610	21	US-10-363-463A-23154	Sequence 23154, A
36	19.4	88.2	838	20	US-10-363-345A-32131	Sequence 32131, A
37	19.4	88.2	838	20	US-10-363-345A-32132	Sequence 32132, A
38	19.4	88.2	838	21	US-10-363-463A-32131	Sequence 32131, A
39	19.4	88.2	838	21	US-10-363-463A-32132	Sequence 32132, A
40	19.4	88.2	839	20	US-10-363-345A-1741	Sequence 1741, Ap
41	19.4	88.2	839	20	US-10-363-345A-1742	Sequence 1742, Ap
42	19.4	88.2	839	21	US-10-363-463A-1741	Sequence 1741, Ap
43	19.4	88.2	839	21	US-10-363-463A-1742	Sequence 1742, Ap
44	19.4	88.2	885	20	US-10-363-345A-18089	Sequence 18089, A
45	19.4	88.2	885	20	US-10-363-345A-18090	Sequence 18090, A
46	19.4	88.2	885	21	US-10-363-463A-18089	Sequence 18089, A
47	19.4	88.2	885	21	US-10-363-463A-18090	Sequence 18090, A
48	19.4	88.2	1267	20	US-10-363-345A-27261	Sequence 27261, A
49	19.4	88.2	1267	20	US-10-363-345A-27262	Sequence 27262, A
50	19.4	88.2	1267	21	US-10-363-463A-27261	Sequence 27261, A
51	19.4	88.2	1267	21	US-10-363-463A-27262	Sequence 27262, A
52	19.4	88.2	16	16	US-10-312-841-2	Sequence 2, Appli
53	19	86.4	23	21	US-10-644-052A-304	Sequence 304, App
54	19	86.4	23	21	US-10-644-052A-323	Sequence 323, App
55	19	86.4	920	20	US-10-363-345A-20285	Sequence 20285, A
56	19	86.4	920	20	US-10-363-345A-20286	Sequence 20286, A
57	19	86.4	920	21	US-10-363-463A-20285	Sequence 20285, A
58	19	86.4	920	21	US-10-363-463A-20286	Sequence 20286, A
59	18.8	85.5	523	20	US-10-363-345A-17495	Sequence 17495, A
60	18.8	85.5	523	20	US-10-363-345A-17496	Sequence 17496, A
61	18.8	85.5	523	21	US-10-363-463A-17495	Sequence 17495, A
62	18.8	85.5	523	21	US-10-363-463A-17496	Sequence 17496, A
63	18.8	85.5	524	20	US-10-363-345A-15599	Sequence 15599, A
64	18.8	85.5	524	20	US-10-363-345A-15600	Sequence 15600, A
65	18.8	85.5	524	21	US-10-363-463A-15599	Sequence 15599, A
66	18.8	85.5	524	21	US-10-363-463A-15600	Sequence 15600, A
67	18.8	85.5	525	20	US-10-363-345A-35507	Sequence 35507, A
68	18.8	85.5	525	20	US-10-363-345A-35508	Sequence 35508, A
69	18.8	85.5	525	21	US-10-363-463A-35507	Sequence 35507, A
70	18.8	85.5	525	21	US-10-363-463A-35508	Sequence 35508, A
71	18.8	85.5	553	20	US-10-363-345A-39041	Sequence 39041, A
72	18.8	85.5	553	20	US-10-363-345A-39042	Sequence 39042, A
73	18.8	85.5	553	21	US-10-363-463A-39041	Sequence 39041, A
74	18.8	85.5	553	21	US-10-363-463A-39042	Sequence 39042, A
75	18.8	85.5	561	20	US-10-363-345A-35971	Sequence 35971, A
76	18.8	85.5	561	20	US-10-363-345A-35972	Sequence 35972, A
77	18.8	85.5	561	21	US-10-363-463A-35971	Sequence 35971, A
78	18.8	85.5	561	21	US-10-363-463A-35972	Sequence 35972, A
79	18.8	85.5	651	20	US-10-363-345A-34913	Sequence 34913, A
80	18.8	85.5	651	20	US-10-363-345A-34914	Sequence 34914, A

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81 18.8 85.5 651 21 US-10-363-483A-34913 Sequence 34913, A
82 18.8 85.5 651 21 US-10-363-483A-34914 Sequence 34914, A
83 18.8 85.5 712 20 US-10-363-345A-27451 Sequence 27451, A
84 18.8 85.5 712 20 US-10-363-345A-27452 Sequence 27452, A
85 18.8 85.5 712 21 US-10-363-483A-27451 Sequence 27451, A
86 18.8 85.5 712 21 US-10-363-483A-27452 Sequence 27452, A
87 18.8 85.5 759 20 US-10-363-345A-3263 Sequence 3263, Ap
88 18.8 85.5 759 20 US-10-363-345A-3264 Sequence 3264, Ap
89 18.8 85.5 759 21 US-10-363-483A-3263 Sequence 3263, Ap
90 18.8 85.5 759 21 US-10-363-483A-3264 Sequence 3264, Ap
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ALIGNMENTS

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RESULT 1
US-10-613-228A-1
; Sequence 1, Application US/10613228A
; Publication No. US20040092472A1
; GENERAL INFORMATION:
; APPLICANT: KRIEG, ARTHUR M
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS FOR STIMULATING IMMUNE RESPONSES
; FILE REFERENCE: C1037.700450S00
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/10/613,228A
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligodeoxynucleotide
US-10-613-228A-1
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Query Match 100.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 TCGTCGTTTTTCGTGCGTTTTT 22
Db 1 TCGTCGTTTTTCGTGCGTTTTT 22
```

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RESULT 2
US-10-816-220-152
; Sequence 152, Application US/10816220
; Publication No. US20040235770A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID OIL-IN-WATER FORMULATIONS AND
; FILE REFERENCE: C1037.70039US01
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US/10/816,220
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/461,903
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 434
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-816-220-152
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Query Match 100.0%; Score 22; DB 20; Length 22;
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Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TCGTCGTTTTTCGTGCGTTTTT 22
Db 1 TCGTCGTTTTTCGTGCGTTTTT 22
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RESULT 3
US-10-644-052A-290
; Sequence 290, Application US/10644052A
; Publication No. US20050059619A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M
; APPLICANT: Samulowitz, Ulrike
; APPLICANT: Vollmer, Joerg
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Ullrich, Marion
; APPLICANT: Lipford, Robert
; APPLICANT: Rankin, Robert
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS
; FILE REFERENCE: C1037.70048US00
; CURRENT APPLICATION NUMBER: US/10/644,052A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,479
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/404,820
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/429,701
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US 60/447,377
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligodeoxynucleotide
US-10-644-052A-290
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Query Match 100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 TCGTCGTTTTTCGTGCGTTTTT 22
Db 1 TCGTCGTTTTTCGTGCGTTTTT 22
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RESULT 4
US-10-363-345A-34257
; Sequence 34257, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berflin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34257
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 34257
US-10-363-345A-34257
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Query Match 92.7%; Score 20.4; DB 20; Length 618;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCGTCGTTTTTCGTGCGTTTTT 22
|||||
DB 98 TCGTCGTTTTTCGTGCGTTTTT 119

RESULT 5
US-10-363-345A-34258/C
; Sequence 34258, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34258
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 34258
US-10-363-345A-34258

Query Match 92.7%; Score 20.4; DB 20; Length 618;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCGTCGTTTTTCGTGCGTTTTT 22
|||||
DB 521 TCGTCGTTTTTCGTGCGTTTTT 500

RESULT 6
US-10-363-483A-34257
; Sequence 34257, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34257
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 34257
US-10-363-483A-34257

Query Match 92.7%; Score 20.4; DB 21; Length 618;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCGTCGTTTTTCGTGCGTTTTT 22
|||||
DB 98 TCGTCGTTTTTCGTGCGTTTTT 119

RESULT 7
US-10-363-483A-34258/C
; Sequence 34258, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34258
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 34258
US-10-363-483A-34258

Query Match 92.7%; Score 20.4; DB 21; Length 618;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCGTCGTTTTTCGTGCGTTTTT 22
|||||
DB 521 TCGTCGTTTTTCGTGCGTTTTT 500

RESULT 8
US-10-363-345A-40287
; Sequence 40287, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40287
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 40287
US-10-363-345A-40287

Query Match 92.7%; Score 20.4; DB 20; Length 619;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCGTCGTTTTTCGTGCGTTTTT 22
|||||
DB 190 TCGTCGTTTTTCGTGCGTTTTT 211

RESULT 9
US-10-363-345A-40288/C
; Sequence 40288, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

```

; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40288
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 40288
US-10-363-345A-40288
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```

Query Match          92.7%; Score 20.4; DB 21; Length 619;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 TCGTCGTTTTTCGTCGCTTTT 22
          |||||
Db      430 TCGTCGTTTTTCGTCGCTTTT 409
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RESULT 10
US-10-363-483A-40287
; Sequence 40287, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40287
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 40287
US-10-363-483A-40287
```

```

Query Match          92.7%; Score 20.4; DB 21; Length 619;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 TCGTCGTTTTTCGTCGCTTTT 22
          |||||
Db      190 TCGTCGTTTTTCGTCGCTTTT 211
```

```

RESULT 11
US-10-363-483A-40288/C
; Sequence 40288, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40288
; LENGTH: 619
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 40288
US-10-363-483A-40288
```

```

Query Match          92.7%; Score 20.4; DB 21; Length 619;
Best Local Similarity 95.5%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 TCGTCGTTTTTCGTCGCTTTT 22
          |||||
Db      430 TCGTCGTTTTTCGTCGCTTTT 409
```

```

RESULT 12
US-10-363-345A-2025
; Sequence 2025, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: B01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2025
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2025
US-10-363-345A-2025
```

```

Query Match          92.7%; Score 20.4; DB 20; Length 761;
Best Local Similarity 95.5%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 TCGTCGTTTTTCGTCGCTTTT 22
          |||||
Db      598 TCGTCGTTTTTCGTCGCTTTT 619
```

```

RESULT 13
US-10-363-345A-2026/C
; Sequence 2026, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: B01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2026
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2026
US-10-363-345A-2026
```

```

Query Match          92.7%; Score 20.4; DB 20; Length 761;
Best Local Similarity 95.5%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
|||||
Db 164 TCGTCGTTTTTCGTCGTTTTT 143

RESULT 14

US-10-363-483A-2025
; Sequence 2025, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2025
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 2025
US-10-363-483A-2025

Query Match 92.7%; Score 20.4; DB 21; Length 761;
Best Local Similarity 95.5%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
|||||
Db 598 TCGTCGTTTTTCGTCGTTTTT 619

RESULT 15

US-10-363-483A-2026/c
; Sequence 2026, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2026
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 2026
US-10-363-483A-2026

Query Match 92.7%; Score 20.4; DB 21; Length 761;
Best Local Similarity 95.5%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
|||||
Db 164 TCGTCGTTTTTCGTCGTTTTT 143

RESULT 16

US-10-363-345A-7203
; Sequence 7203, Application US/10363345A

; Publication No. US20040234960A1

; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 7203
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 7203
US-10-363-345A-7203

Query Match 92.7%; Score 20.4; DB 20; Length 1024;
Best Local Similarity 95.5%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
|||||
Db 276 TCGTCGTTTTTCGTCGTTTTT 297

RESULT 17

US-10-363-345A-7204/c
; Sequence 7204, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 7204
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 7204
US-10-363-345A-7204

Query Match 92.7%; Score 20.4; DB 20; Length 1024;
Best Local Similarity 95.5%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
|||||
Db 749 TCGTCGTTTTTCGTCGTTTTT 728

RESULT 18

US-10-363-483A-7203
; Sequence 7203, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A

;; CURRENT FILING DATE: 2003-03-03
;; NUMBER OF SEQ ID NOS: 40712
;; SEQ ID NO 7203
;; LENGTH: 1024
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;; OTHER INFORMATION: Cpg-island No: 7203
US-10-363-483A-7203

Query Match 92.7%; Score 20.4; DB 21; Length 1024;
Best Local Similarity 95.5%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGCGCTTTT 22
DB 276 TCGTCGTTGTTTCGCGCTTTT 297

RESULT 19

US-10-363-483A-7204/C
; Sequence 7204, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 7204
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 7204
US-10-363-483A-7204

Query Match 92.7%; Score 20.4; DB 21; Length 1024;
Best Local Similarity 95.5%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGCGCTTTT 22
DB 749 TCGTCGTTGTTTCGCGCTTTT 728

RESULT 20

US-10-363-345A-28015
; Sequence 28015, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-Cpg-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28015
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 28015

QY 1 TCGTCGTTTTTCGCGCTTTT 22
DB 474 TCGTCGTTGTTTCGCGCTTTT 494

US-10-363-345A-28015

Query Match 88.2%; Score 19.4; DB 20; Length 511;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGTCGTTTTTCGCGCTTTT 22
DB 474 CGTCGTTTTTCGCGCTTTT 494

RESULT 21

US-10-363-345A-28016/C
; Sequence 28016, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-Cpg-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28016
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 28016
US-10-363-345A-28016

Query Match 88.2%; Score 19.4; DB 20; Length 511;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGTCGTTTTTCGCGCTTTT 22
DB 38 CGTCGTTTTTCGCGCTTTT 18

RESULT 22

US-10-363-483A-28015
; Sequence 28015, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28015
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 28015
US-10-363-483A-28015

Query Match 88.2%; Score 19.4; DB 21; Length 511;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGTCGTTTTTCGCGCTTTT 22
DB 474 CGTCGTTTTTCGCGCTTTT 494

```
RESULT 23
US-10-363-483A-28016/c
; Sequence 28016, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28016
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 28016
US-10-363-483A-28016

Query Match      88.2%; Score 19.4; DB 21; Length 511;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CGTCGTTTTTCGTCGCTTTT 22
Db      38 CGTCGTTTTTCGCGCGCTTTT 18

RESULT 24
US-10-363-345A-35059
; Sequence 35059, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35059
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 35059
US-10-363-345A-35059

Query Match      88.2%; Score 19.4; DB 20; Length 523;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CGTCGTTTTTCGTCGCTTTT 22
Db      488 CGTCGTTTTTCGTCGCTTTT 508

RESULT 25
US-10-363-345A-35060/c
; Sequence 35060, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35060
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 35060
US-10-363-345A-35060

Query Match      88.2%; Score 19.4; DB 20; Length 523;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CGTCGTTTTTCGTCGCTTTT 22
Db      36 CGTCGTTTTTCGTCGCTTTT 16

RESULT 26
US-10-363-483A-35059
; Sequence 35059, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35059
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 35059
US-10-363-483A-35059

Query Match      88.2%; Score 19.4; DB 21; Length 523;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CGTCGTTTTTCGTCGCTTTT 22
Db      488 CGTCGTTTTTCGTCGCTTTT 508

RESULT 27
US-10-363-483A-35060/c
; Sequence 35060, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35060
; LENGTH: 523
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 35060
US-10-363-483A-35060
```

```
Query Match      88.2%; Score 19.4; DB 21; Length 523;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CGTCGTTTTTCGTCGTTTTT 22
        |||||
Db      36 CGTCGTTTTTCGTCGTTTTT 16
```

```
RESULT 28
US-10-363-345A-40325
; Sequence 40325, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; NUMBER OF SEQ ID NOS: 2003-03-03
; SEQ ID NO 40325
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 40325
US-10-363-345A-40325
```

```
Query Match      88.2%; Score 19.4; DB 20; Length 524;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CGTCGTTTTTCGTCGTTTTT 22
        |||||
Db      399 CGTCGTTTTTCGTCGTTTTT 419
```

```
RESULT 29
US-10-363-345A-40326/c
; Sequence 40326, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; NUMBER OF SEQ ID NOS: 2003-03-03
; SEQ ID NO 40326
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 40326
US-10-363-345A-40326
```

```
Query Match      88.2%; Score 19.4; DB 20; Length 524;
Best Local Similarity 95.2%; Pred. No. 80;
```

```
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      2 CGTCGTTTTTCGTCGTTTTT 22
        |||||
Db      126 CGTCGTTTTTCGTCGTTTTT 106
```

```
RESULT 30
US-10-363-483A-40325
; Sequence 40325, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; NUMBER OF SEQ ID NOS: 2003-03-03
; SEQ ID NO 40325
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 40325
US-10-363-483A-40325
```

```
Query Match      88.2%; Score 19.4; DB 21; Length 524;
Best Local Similarity 95.2%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CGTCGTTTTTCGTCGTTTTT 22
        |||||
Db      399 CGTCGTTTTTCGTCGTTTTT 419
```

```
Search completed: August 29, 2005, 00:03:33
Job time : 376 secs
```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2005, 20:09:59 , Search time 64 Seconds
(without alignments)
562.470 Million cell updates/sec

Title: US-10-613-228a-1

Perfect score: 12
Sequence: 1 tgcgcgttttcgtcgttttc 22

Scoring table: IDENTITY NUC
Gap 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database:

Issued Patents NA: *
1: /cgn2_6/ptodaca/1/ina/5A COMB.seq: *
2: /cgn2_6/ptodaca/1/ina/5B COMB.seq: *
3: /cgn2_6/ptodaca/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodaca/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodaca/1/ina/PCTUS COMB.seq: *
6: /cgn2_6/ptodaca/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	17.2	78.2	133 4 US-09-313-294A-108	Sequence 108, App
2	17.2	78.2	513 4 US-09-107-532A-292	Sequence 292, App
3	16.8	76.4	36016 4 US-09-949-016-14223	Sequence 14223, A
4	16.4	74.5	3531 1 US-08-629-600-1	Sequence 1, Appl1
5	16.4	74.5	3531 3 US-09-076-761-1	Sequence 1, Appl1
6	16.2	73.6	909 4 US-09-134-000C-3167	Sequence 3167, Ap
7	16.2	73.6	2358 4 US-09-134-000C-3285	Sequence 3285, Ap
8	15.8	71.8	660 4 US-09-489-039A-560	Sequence 560, App
9	15.8	70.9	231 4 US-09-543-681A-2772	Sequence 2772, Ap
10	15.6	70.9	300 4 US-09-543-681A-1478	Sequence 1478, Ap
11	15.6	70.9	440 4 US-09-513-999C-35185	Sequence 35185, A
12	15.6	70.9	599 4 US-09-270-767-3552	Sequence 3552, Ap
13	15.6	70.9	599 4 US-09-270-767-18834	Sequence 18834, A
14	15.6	70.9	601 4 US-09-949-016-11352	Sequence 11352, A
15	15.6	70.9	601 4 US-09-949-016-69221	Sequence 69221, A
16	15.6	70.9	601 4 US-09-949-016-81370	Sequence 81370, A
17	15.6	70.9	601 4 US-09-949-016-127440	Sequence 127440, A
18	15.6	70.9	601 4 US-09-949-016-177125	Sequence 177125, A
19	15.6	70.9	601 4 US-09-949-016-177126	Sequence 177126, A
20	15.6	70.9	601 4 US-09-949-016-177127	Sequence 177127, A
21	15.6	70.9	678 3 US-09-134-001C-2551	Sequence 2551, Ap
22	15.6	70.9	826 3 US-09-221-017B-1008	Sequence 1008, Ap
23	15.6	70.9	850 3 US-08-617-860B-34	Sequence 34, Appl
24	15.6	70.9	1068 4 US-09-543-681A-2972	Sequence 2972, Ap
25	15.6	70.9	1734 4 US-09-248-796A-1704	Sequence 1704, Ap
26	15.6	70.9	2109 4 US-09-248-796A-2999	Sequence 2999, Ap
27	15.6	70.9	2394 4 US-09-540-236-893	Sequence 893, App

28	15.6	70.9	3069 3 US-08-335-865U-7	Sequence 7, Appl1
29	15.6	70.9	3805 3 US-09-513-729B-10	Sequence 10, Appl
30	15.6	70.9	3805 4 US-09-023-655-1443	Sequence 1443, Ap
31	15.6	70.9	4071 3 US-09-513-057C-5	Sequence 5, Appl1
32	15.6	70.9	4071 4 US-09-746-801A-5	Sequence 5, Appl1
33	15.6	70.9	4285 4 US-09-949-016-689	Sequence 689, App
34	15.6	70.9	4308 4 US-09-394-142B-23	Sequence 23, Appl
35	15.6	70.9	4643 2 US-08-605-106-6	Sequence 6, Appl1
36	15.6	70.9	5061 3 US-09-355-160D-1	Sequence 1, Appl1
37	15.6	70.9	5061 4 US-10-092-219-1	Sequence 1, Appl1
38	15.6	70.9	5296 4 US-09-949-016-2362	Sequence 2362, Ap
39	15.6	70.9	8302 3 US-09-234-827B-1	Sequence 1, Appl1
40	15.6	70.9	10204 4 US-09-949-016-14104	Sequence 14104, A
41	15.6	70.9	10482 3 US-09-322-478-23	Sequence 23, Appl
42	15.6	70.9	10482 4 US-09-586-106D-23	Sequence 23, Appl
43	15.6	70.9	14066 4 US-09-601-198-56	Sequence 56, Appl
44	15.6	70.9	26709 4 US-09-949-016-17520	Sequence 17520, A
45	15.6	70.9	34279 4 US-09-596-002-26	Sequence 26, Appl
46	15.6	70.9	43657 4 US-09-949-016-13777	Sequence 13777, A
47	15.6	70.9	46899 1 US-08-471-119A-1	Sequence 1, Appl1
48	15.6	70.9	47683 4 US-09-949-016-16460	Sequence 16460, A
49	15.6	70.9	57507 4 US-09-949-016-15019	Sequence 15019, A
50	15.6	70.9	92304 4 US-09-949-016-15943	Sequence 15943, A
51	15.6	70.9	92344 4 US-09-949-016-16802	Sequence 16802, A
52	15.6	70.9	106418 4 US-09-949-016-13974	Sequence 13974, A
53	15.6	70.9	111235 4 US-09-949-016-15328	Sequence 15328, A
54	15.6	70.9	124480 4 US-09-949-016-15921	Sequence 15921, A
55	15.6	70.9	126176 4 US-09-949-016-16137	Sequence 16137, A
56	15.6	70.9	126176 4 US-09-949-016-16138	Sequence 16138, A
57	15.6	70.9	129327 4 US-09-949-016-12657	Sequence 12657, A
58	15.6	70.9	129327 4 US-09-949-016-15368	Sequence 15368, A
59	15.6	70.9	228851 4 US-09-949-016-13781	Sequence 13781, A
60	15.6	70.9	250715 4 US-09-949-016-13294	Sequence 13294, A
61	15.6	70.9	640681 4 US-09-790-988-1	Sequence 1, Appl1
62	15.4	70.0	3585 4 US-09-270-767-14479	Sequence 14479, A
63	15.4	70.0	119930 4 US-09-949-016-12677	Sequence 12677, A
64	15.4	70.0	119931 4 US-09-949-016-16319	Sequence 16319, A
65	15.4	70.0	12536 4 US-09-949-016-1486	Sequence 1486, A
66	15.2	69.1	405 4 US-09-328-352-1456	Sequence 1456, Ap
67	15.2	69.1	601 4 US-09-949-016-29225	Sequence 29225, A
68	15.2	69.1	601 4 US-09-949-016-41521	Sequence 41521, A
69	15.2	69.1	601 4 US-09-949-016-131612	Sequence 131612, A
70	15.2	69.1	601 4 US-09-949-016-187998	Sequence 187998, A
71	15.2	69.1	627 3 US-08-598-416-53	Sequence 53, Appl
72	15.2	69.1	636 4 US-09-134-000C-789	Sequence 789, App
73	15.2	69.1	1466 3 US-09-130-242-8	Sequence 8, Appl1
74	15.2	69.1	1466 4 US-09-583-610D-8	Sequence 8, Appl1
75	15.2	69.1	2371 4 US-09-270-767-14386	Sequence 14386, A
76	15.2	69.1	2670 4 US-09-583-110-1789	Sequence 1789, Ap
77	15.2	69.1	2670 4 US-09-107-433-2144	Sequence 2144, Ap
78	15.2	69.1	2834 4 US-09-566-921-43	Sequence 43, Appl
79	15.2	69.1	3078 4 US-09-270-767-13793	Sequence 13793, A
80	15.2	69.1	3579 4 US-09-134-000C-1439	Sequence 1439, Ap
81	15.2	69.1	3755 4 US-09-949-016-2724	Sequence 2724, Ap
82	15.2	69.1	3755 4 US-09-949-016-1064	Sequence 1064, Ap
83	15.2	69.1	3773 3 US-09-130-242-1	Sequence 1, Appl1
84	15.2	69.1	3773 4 US-09-583-610D-1	Sequence 1, Appl1
85	15.2	69.1	6755 3 US-08-931-999-4	Sequence 4, Appl1
86	15.2	69.1	8280 4 US-09-949-016-12806	Sequence 12806, A
87	15.2	69.1	8283 4 US-09-949-016-14466	Sequence 14466, A
88	15.2	69.1	10223 3 US-08-961-527-73	Sequence 73, Appl
89	15.2	69.1	10223 4 US-09-949-016-12316	Sequence 12316, A
90	15.2	69.1	39233 4 US-09-949-016-12316	Sequence 12316, A

RESULT 1
US-09-313-294A-108
; Sequence 108, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:

ALIGNMENTS

APPLICANT: Laligudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 108
LENGTH: 133
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700548545H1
NAME/KEY: unsure
LOCATION: 8
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-108

Query Match 78.2%; Score 17.2; DB 4; Length 133;
Best Local Similarity 86.4%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTCGTCGCTTTT 22
|||||
Db 72 TCGTCGTTTTCGTCGCTTTT 93

RESULT 2
US-09-107-532A-292/C
Sequence 292, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucetee-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Walcham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arianello, Pamela Deneka

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 292:

SEQUENCE CHARACTERISTICS:

LENGTH: 513 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...513
SEQUENCE DESCRIPTION: SEQ ID NO: 292:
US-09-107-532A-292

Query Match 78.2%; Score 17.2; DB 4; Length 513;
Best Local Similarity 86.4%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTCGTCGCTTTT 22
|||||
Db 76 TCGTCGTTTTCGTCGCTTTT 55

RESULT 3
US-09-949-016-14223/C
Sequence 14223, Application US/09949016
Patent No. 6812338

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14223

LENGTH: 36016

TYPE: DNA

ORGANISM: Human

US-09-949-016-14223

Query Match 76.4%; Score 16.8; DB 4; Length 36016;
Best Local Similarity 90.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTCGTTTTCGTCGCTTTT 22
|||||
Db 31422 GTCGTTTTCGTCGCTTTT 31403

RESULT 4
US-08-629-600-1/C
Sequence 1, Application US/08629600
Patent No. 5783196

GENERAL INFORMATION:

APPLICANT: NORIEGA, Fernando

APPLICANT: LEVINE, Myron M.

TITLE OF INVENTION: GUA MUTANTS OF SHIGELLA
AND VACCINES CONTAINING THE SAME

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W., Suite 800

CITY: Washington, D.C.

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,600
FILING DATE: 9-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-629-600-1

Query Match
Best Local Similarity 74.5%; Score 16.4; DB 1; Length 3531;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGTTTTCGTGCGTTT 22
DB 846 CGTTTTCGTGCGTTT 829

RESULT 5
US-09-076-761-1/c
Sequence 1, Application US/09076761
Patent No. 6190669
GENERAL INFORMATION:
APPLICANT: NORIEGA, Fernando
APPLICANT: SZTEIN, Marcelo B.
APPLICANT: LEVINE, Myron M.
TITLE OF INVENTION: ATTENUATED MUTANTS OF SALMONELLA
TITLE OF INVENTION: WHICH CONSTITUTIVELY EXPRESS THE
TITLE OF INVENTION: VI ANTIGEN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPHEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,761
FILING DATE: 13-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-7140
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7860
TELEFAX: (202) 293-7060
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-076-761-1

Query Match
Best Local Similarity 74.5%; Score 16.4; DB 3; Length 3531;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGTTTTCGTGCGTTT 22
DB 846 CGTTTTCGTGCGTTT 829

RESULT 6
US-09-134-000C-3167/c
Sequence 3167, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3167
LENGTH: 909
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-3167

Query Match
Best Local Similarity 73.6%; Score 16.2; DB 4; Length 909;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTCGTTTTCGTGCGTTT 22
DB 248 CGTCGTTTTCGTGCGTTT 228

RESULT 7
US-09-134-000C-3285/c
Sequence 3285, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3285
LENGTH: 2358
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-3285

Query Match
Best Local Similarity 73.6%; Score 16.2; DB 4; Length 2358;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTCGTTTTCGTGCGTTT 22
DB 1697 CGTCGTTTTCGTGCGTTT 1677


```
RESULT 13
US-09-270-767-18834/c
; Sequence 18834, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 18834
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-18834

Query Match
Best Local Similarity 70.9%; Score 15.6; DB 4; Length 599;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 568 TCGTCGTCGTCGTCGTCGTTTTT 547

RESULT 14
US-09-949-016-31352/c
; Sequence 31352, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31352
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-31352

Query Match
Best Local Similarity 70.9%; Score 15.6; DB 4; Length 601;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 334 TCGTCGTTTTTCGTCGTTTTT 313

RESULT 15
US-09-949-016-69221/c
; Sequence 69221, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69221
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-69221

Query Match
Best Local Similarity 70.9%; Score 15.6; DB 4; Length 601;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 416 TCGTCGTTTTTCGTCGTTTTT 395

RESULT 16
US-09-949-016-81370/c
; Sequence 81370, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81370
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-81370

Query Match
Best Local Similarity 70.9%; Score 15.6; DB 4; Length 601;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 334 TCGTCGTTTTTCGTCGTTTTT 313

RESULT 17
US-09-949-016-127420/c
; Sequence 127420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 127420
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-127420

Query Match
Best Local Similarity 81.8%; Score 15.6; DB 4; Length 601;
Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
DB 330 TCCTCCTTTTCTTCTGCTTTTT 309

RESULT 18
US-09-949-016-177125/c
Sequence 177125, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 177125
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-177125

Query Match
Best Local Similarity 81.8%; Score 15.6; DB 4; Length 601;
Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
DB 146 TCGTCGATCTCTGCGTTTTT 125

RESULT 19
US-09-949-016-177126/c
Sequence 177126, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 177126

LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-177126

Query Match
Best Local Similarity 81.8%; Score 15.6; DB 4; Length 601;
Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
DB 183 TCCTCCATCTCTGCGTTTTT 162

RESULT 20
US-09-949-016-177127/c
Sequence 177127, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 177127
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-177127

Query Match
Best Local Similarity 81.8%; Score 15.6; DB 4; Length 601;
Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
DB 426 TCGTCGATCTCTGCGTTTTT 405

RESULT 21
US-09-134-001C-2551/c
Sequence 2551, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2551
LENGTH: 678
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2551

Query Match
Best Local Similarity 81.8%; Score 15.6; DB 3; Length 678;
Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

;; CURRENT APPLICATION NUMBER: US/09/543,681A
;; CURRENT FILING DATE: 2000-04-05
;; PRIOR APPLICATION NUMBER: US 60/128,706
;; PRIOR FILING DATE: 1999-04-09
;; NUMBER OF SEQ ID NOS: 8344
;; SEQ ID NO 2972
;; LENGTH: 1068
;; TYPE: DNA
;; ORGANISM: Proteus mirabilis
US-09-543-681A-2972

Query Match 70.9%; Score 15.6; DB 4; Length 1068;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGCGTTTTTCGCGCTTTT 22
DB 135 TCGCGTTTTTCGCGCTTTT 114

RESULT 25

US-09-248-796A-4704/C
;; Sequence 4704, Application US/09248796A
;; Patent No. 6747137
;; GENERAL INFORMATION:
;; APPLICANT: Keith Weinstock et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 4704
;; LENGTH: 1734
;; TYPE: DNA
;; ORGANISM: Candida albicans
US-09-248-796A-4704

Query Match 70.9%; Score 15.6; DB 4; Length 1734;
Best Local Similarity 81.8%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGCGTTTTTCGCGCTTTT 22
DB 398 TCGCGTTTTTCGCGCTTTT 377

RESULT 26

US-09-248-796A-2999
;; Sequence 2999, Application US/09248796A
;; Patent No. 6747137
;; GENERAL INFORMATION:
;; APPLICANT: Keith Weinstock et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 2999
;; LENGTH: 2109
;; TYPE: DNA
;; ORGANISM: Candida albicans
US-09-248-796A-2999

Query Match 70.9%; Score 15.6; DB 4; Length 2109;
Best Local Similarity 81.8%; Pred. No. 7.2e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGCGTTTTTCGCGCTTTT 22
DB 247 TCGCGTTTTTCGCGCTTTT 268

RESULT 27

US-09-540-236-893/C
;; Sequence 893, Application US/09540236
;; Patent No. 6673910
;; GENERAL INFORMATION:
;; APPLICANT: Gary L. Breton et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 2709.2005-001
;; CURRENT APPLICATION NUMBER: US/09/540,236
;; CURRENT FILING DATE: 2000-04-04
;; NUMBER OF SEQ ID NOS: 3840
;; SEQ ID NO 893
;; LENGTH: 2394
;; TYPE: DNA
;; ORGANISM: M. catarrhalis
US-09-540-236-893

Query Match 70.9%; Score 15.6; DB 4; Length 2394;
Best Local Similarity 81.8%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGCGTTTTTCGCGCTTTT 22
DB 1232 TCGCGTTTTTCGCGCTTTT 1211

RESULT 28

US-08-335-865J-7
;; Sequence 7, Application US/08335865J
;; Patent No. 6107472
;; GENERAL INFORMATION:
;; APPLICANT: Stacker, Steven A.; Hovens, Christopher M.,
;; APPLICANT: Wilks, Andrew F.
;; TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: Fulbright & Jaworski L.L.P.
;; STREET: 666 Fifth Ave
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10103

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: ASCII/Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/335,865J
;; FILING DATE: 19-January-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/AU93/00210
;; FILING DATE: 10-May-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP2358
;; FILING DATE: 11-May-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 6107472man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD-5277
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 318-3100

TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3069
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-335-8650-7

Query Match 70.9%; Score 15.6; DB 3; Length 3069;
 Best Local Similarity 81.8%; Pred. No. 7.4e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
 DB 2273 TTGTCGTTTTTTGTGTCGTTTTT 2252

RESULT 29
 US-09-513-7298-10/c
 Sequence 10, Application US/095137298
 Patent No. 6165791
 GENERAL INFORMATION:
 APPLICANT: Ian Popoff
 TITLE OF INVENTION: ANTISENSE MODULATION OF B2F TRANSCRIPTION FACTOR 3 EXPRESSION
 FILE REFERENCE: RTS-0112
 CURRENT APPLICATION NUMBER: US/09/513,7298
 CURRENT FILING DATE: 2000-02-24
 NUMBER OF SEQ ID NOS: 88
 SEQ ID NO 10
 LENGTH: 3805
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(525)
 US-09-513-7298-10

Query Match 70.9%; Score 15.6; DB 3; Length 3805;
 Best Local Similarity 81.8%; Pred. No. 7.5e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
 DB 2273 TTGTCGTTTTTTGTGTCGTTTTT 2252

RESULT 30
 US-09-023-655-1443/c
 Sequence 1443, Application US/09023655
 Patent No. 6607879
 GENERAL INFORMATION:
 APPLICANT: Cocks, Benjamin G.
 APPLICANT: Susan G. Stuart
 APPLICANT: Jeffrey J. Seilhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 TITLE OF INVENTION: EXPRESSION
 NUMBER OF SEQUENCES: 1508
 CORRESPONDENCE ADDRESS:
 ADDRESS: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1443:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3805 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 9559708
 US-09-023-655-1443

Query Match 70.9%; Score 15.6; DB 4; Length 3805;
 Best Local Similarity 81.8%; Pred. No. 7.5e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
 DB 2273 TTGTCGTTTTTTGTGTCGTTTTT 2252

Search completed: August 28, 2005, 22:57:21
 Job time : 68 secs

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